

AMENDMENTS TO THE SPECIFICATION

Delete the existing sequence listing and insert the accompanying sequence listing (pages 1-212).

Delete the existing formal drawings (Figures 1A, 1B, 1C, 2A, 2B, 3, 4A, 4B, and 5) and insert the accompanying 9 sheets of replacement formal drawings ((Figures 1A, 1B, 1C, 2A, 2B, 3, 4A, 4B, and 5).

Delete the existing Table 3 at page 20 and insert the following replacement Table 3:

Table 3. Illustration of the design of the conformation determining regions and protease binding sites in molecules having P domains larger than 4 amino acids. The P1 residue is underlined. Z is benzyloxycarbonyl group, K[TFA] means Lys(N(epsilon)trifluoroacetyl), Fm is Fmoc (preferably attached to the alpha amino group of the amino terminal residue *e.g.*, Lysine (K)). O indicates tetrahydroisoquinoline-3-carboxylic acid. Aib, designated as B, can be replaced by Pro.

Name	aa ¹	aa ² - aa ³	aa ⁴	aa ⁵	X	P	Y	aa ⁶	aa ⁷	aa ⁸ - aa ⁹	aa ¹⁰	S ²	SEQ ID NO
PAI-2	K	D		B		TGR <u>T</u> G		P			K	GY	1
PAI-2(b)	K	D	P	P		TGR <u>T</u> G		P	P		K	GY	2
DEV <u>D</u>	K	D		B		DEV <u>D</u> GID		P			K	GY	3
Dev <u>N</u>	K	D		B		DEV <u>N</u> GID		P			K	GY	4
PAR <u>P</u>	K	D		B		EVD <u>P</u> GID		P			K	GY	5
ICE	K	DY		B		A <u>D</u> GID		P			K	GY	6
Fm-DEV <u>D</u>	Fm-K	D		B		DEV <u>D</u> GID		P			K	GY	7
Fm-DEV <u>N</u>	Fm-K	D		B		DEV <u>N</u> GID		P			K	GY	8
Fm-PAR <u>P</u>	Fm-K	D		B		EVD <u>P</u> GID		P			K	GY	9
Fm-KNFES	Fm-K	D		-		AIP <u>M</u> SI		P			K	GY	10
	Fm-K	D				AIPN <u>l</u> uSI		P			K	GY	11
Fm-G2D2D	Fm-K	D		B		GDEV <u>D</u> GID	G	P			K	GY	12
Fm-CGD2D	Fm-K	D		B	J	GDEV <u>D</u> GID	GJ	P			K	GY	13
Z-CGD2D	Z-K	D		B	J	GDEV <u>D</u> GID	GJ	P			K	GY	14
Fm-ICE	Fm-K	DY		B		A <u>D</u> GID		P			K	GY	15

Delete the existing Table 4 at pages 21-29 and insert the following replacement Table 4:

Table 4. Illustration of the design of the conformation determining regions and protease binding sites in molecules having P domains larger than 4 amino acids. The P1 residue is underlined. Z is benzyloxycarbonyl group, K[TFA] means Lys(N(epsilon)trifluoroacetyl), Fm is Fmoc (preferably attached to the alpha amino group of the amino terminal residue *e.g.*, Lysine (K). O indicates tetrahydroisoquinoline-3-carboxylic acid. Aib, designated as B, can be replaced by Pro. J is epsilon-aminocaproic acid.

Substrate class	aa ¹	aa ² -aa ³	aa ⁴	aa ⁵	X	P	Y	aa ⁶	aa ⁷	aa ⁸ -aa ⁹	aa ¹⁰	S ²	SEQ ID NO
CPP32 substrates (preferably with DER and TMR fluorophores). Note where Fmoc (Fm) is indicated, it is optional, and where not indicated it can be added.													
	Fa-K	D		P	JG	DEV <u>D</u> GIN	GJ	P			K	GY	261
	Fm-K	D		P	JG	DEV <u>D</u> GIN	GJ	P			K amid e		262
	Fm-K	D		P	JG	(d-O)DEV <u>D</u> GIN	GJ	P			K	GY	263
	Fm-K	D		P	JG	DEV <u>D</u> GIN	G	P			K	GY	264
	Fm-K	D		P	G	DEV <u>D</u> GIN	GJ	P			K	GY	265
	Fm-K	D		P	JG	DEV <u>D</u> GID	GJ	P			K amid e		266
	Fm-K	D		P	JG	EEVEGIN	GJ	P			K	GY	267
	Fm-K	D		P	JG	D(dF)VD <u>G</u> IN	GJ	P			K	GY	268
	Fm-K	D		P	JG	(d-D)EV(d-D) <u>G</u> IN	GJ	P			K	GY	269
	Fm-K	D		P	JG	DEV <u>D</u> GIN	GJ	P			K	GY	270
	Fm-K	DB			JG	DEV <u>N</u> GIN	GJ	P			K	GY	271
	Fm-K	DB			JG	DEV <u>D</u> GID	GJ	P			K	GY	272
	Fm-	DB			JG	DEV <u>D</u> GIN	GJ	P			K	GY	273

	K												
	Fm-K	DB			JG	DEV <u>N</u> GID	GJ	P			K	GY	274
	K	D		B	JJ	GDEV <u>D</u> GID	JJ	P			K	GY	275
	K	D		B	J	GNEV <u>D</u> GID	GJ	P			K	GY	276
	K	D		B	J	GDEV <u>D</u> GIN	GJ	P			K	GY	277
	K	D		B	J	GNEV <u>D</u> GIN	GJ	P			K	GY	278
	K	D		B	J	GDEV <u>N</u> GIN	GJ	P			K	GY	279
	K	D		B	J	GNEV <u>N</u> GIN	GJ	P			K	GY	280
	K	D		B	JG	ODEV <u>D</u> GID	GJ	P			K	GK	281
	K	D		B	JG	dODEV <u>D</u> GI D	GJ	P			K	GY	282
	K	D		B	JG	WDEV <u>D</u> GI D	GJ	P			K	GY	283
	K	D		B	JG	dWDEV <u>D</u> GI D	GJ	P			K	GY	284
	K	D		B	JG	dOdODEV <u>D</u> GID	GJ	P			K	GY	285
	K	D		B	JG	dWdWDEV <u>D</u> GID	GJ	P			K	GY	286
	K	D		B		YVAD <u>G</u> ID		P			K	GY	287
	K	D		B		YVAD <u>G</u> IN		P			K	GY	288
	K	D		B		YV <u>A</u> GIN		P			K	GY	289
	K	D		B	G	YVAD <u>G</u> ID	G	P			K	GY	290
	K	D		B	G	YVAD <u>G</u> IN	G	P			K	GY	291
	K	D		B	G	YV <u>A</u> GIN	G	P			K	GY	292
	K	D		B	JG	YVAD <u>G</u> ID	GJ	P			K	GY	293
	K	D		B	JG	YV <u>A</u> GID	GJ	P			K	GY	294
	K	D		B	JG	YV <u>A</u> GIN	GJ	P			K	GY	295
	K	D		B	JG	YVAD <u>G</u> IN	GJ	P			K	GY	296
	K	D		B	JG	dYVAD <u>G</u> IN	GJ	P			K	GY	297
LAMIN-A													
	Fm-K	D		P	JG	LVEIDNG	J	P			K	GY	298

	Fm-K	DP			JG	LVEIENG	J	P			K	GY	299
	K	D		B		LVEIDNG		P			K	GY	300
	K	D		B	G	LVEIDNG	G	P			K	GY	301
	K	D		B	JG	LVEIDNG	GJ	P			K	GY	302
	K	D		B	JG	LVEINNG	GJ	P			K	GY	303
ProCPP32Asp175													
	Fm-K	D		P	J	GIETESGV	GJ	P			K	GY	304
	Fm-K	D		P	J	GIETDSG	J	P			K	GY	305
	Fm-K	D		P	J	GIETESG	J	P			K	GY	306
	K	D		B		GIETDSGV DD		P			K	GY	307
	K	D		B		GIETNSGV DD		P			K	GY	308
	K	D		B	G	GIETDSGV DD	G	P			K	GY	309
	K	D		B	G	GIETNSGV	G	P			K	GY	310
	K	D		B	J	GIETDSGV	J	P			K	GY	311
	K	D		B	J	GIETNSGV	J	P			K	GY	312
	K	D		B	JG	GIETDSGV	GJ	P			K	GY	313
	K	D		B	JG	GIETNSGV	GJ	P			K	GY	314
ProCPP32Asp28													
	K	D		B		GSESMDSG ISLD		P			K	GY	315
	K	D		B	G	GSESMDSG	G	P			K	GY	316
	K	D		B	JG	GSESMDSG	GJ	P			K	GY	317
NS3 NS5A/5B													
	K	D		B	JG	DVVCCSM S	GJ	P			K	GY	318
	K	D		B	JG	DVVCDSM S	GJ	P			K	GY	319
	K	D		B	JG	DVVCCSdM	GJ	P			K	GY	320

						S							
	K	D		B	JG	DVVCD <u>S</u> d MS	GJ	P			K	GY	321
	K	D		B	JG	DVVCC <u>P</u> dM S	GJ	P			K	GY	322
	K	D		B	JG	EDVVCC <u>S</u>	GJ	P			K	GY	323
	K	D		B	JG	EDVVCD <u>S</u>	GJ	P			K	GY	324
	K	D		B	JG	EDdVVCC <u>P</u>	GJ	P			K	GY	325
	K	D		B	JG	EDdVVCD <u>P</u>	GJ	P			K	GY	326
	K	D		B	JG	DdVVCC <u>S</u> d MS	GJ	P			K	GY	327
	K	D		B	JG	DVdVCD <u>S</u> d MS	GJ	P			K	GY	328
	K	D		B	JG	DdVVCC <u>P</u> d MS	GJ	P			K	GY	329
	K	D		B	JG	DVVCC <u>S</u> M	GJ	P			K	GY	330
	K	D		B	JG	DVVCD <u>S</u> M	GJ	P			K	GY	331
	K	D		B	JG	VCC <u>S</u> M	GJ	P			K	GY	332
	K	D		B	JG	VCD <u>S</u> M	GJ	P			K	GY	333
NS3 NS4A/4B													
	K	D		B	JG	DEMEEC <u>S</u> Q HL		P			K	GY	334
	K	D		B	JG	DEMEEC <u>P</u> Q HL		P			K	GY	335
	K	D		B	JG	DEMEED <u>S</u> Q HL		P			K	GY	336
	K	D		B	JG	EMEEC <u>S</u> QH L		P			K	GY	337
	K	D		B	JG	EMEEC <u>P</u> QH L		P			K	GY	338
	K	D		B	JG	EMEED <u>S</u> QH L		P			K	GY	339
	K	D		B	JG	EMEEC <u>S</u> QH L	G	P			K	GY	340
	K	D		B	JG	EMEEC <u>P</u> QH L	G	P			K	GY	341

	K	D		B	JG	EMEEDSQH L	G	P			K	GY	342
	K	D		B	JG	EMEEC SQH L	GJ	P			K	GY	343
	K	D		B	JG	EMEEC PQH L	GJ	P			K	GY	344
	K	D		B	JG	EMEEDSQH L	GJ	P			K	GY	345
Ext. PAI-2													
	K	D		B	JG	VMTGRTG	J	P			K	GY	346
	K	D		B	JG	VdMTGRTG	J	P			K	GY	347
	K	D		B	JG	VMTGRTG	J	P			K	GY	348
	K	D		B	JG	VMTGRTG	J	P			K	GY	349
THROMB													
	K	D		B	JG	VMTGRG	J	P			K	GY	350
	K	D		B	JG	VMTGRG	GJ	P			K	GY	351
	K	D		B	JG	VdmTGRG	GJ	P			K	GY	352
Urokinase													
	Fm-K	D		P	J	TGRT							353
		Fm-D		P		TGRT	G	P			K	GY	354
	Fm-K	D		P		VMTGRT	GJ	P			K	GY	355
	Fm-K	D		P		TGRT	GJ	P			K	GY	356
	Fm-K	D		P	JG	TGRT	GJ	P			K	GY	357
	Fm-K	D		P	JG	TGRT	G	P			K	GY	358
	Fm-K	D		P	G	TGRT	G	P			K	GY	359
	K	D		P	J	TGRTG	J	P			K	GY	360
	K	D		P	C3	TGRTG		P			K	GY	361
	K	D		P	C7	TGRTG		P			K	GY	362

	K	D		B	JG	VM <u>TGR</u> VG	J	P			K	GY	363
	K	D		B	JG	VdMT <u>G</u> RV G	J	P			K	GY	364
F12A													
	K	D		B	JG	VM <u>TGR</u> AG	J	P			K	GY	365
	K	D		B	JG	VdMT <u>G</u> RA G	J	P			K	GY	366
Swedish KM/NL AMLOID													
	Fm- K	D		P	JG	SEVKLDAE F GC5PKG	GJ	P			K	GY	367
	Fm- K	D		P	JG	S(d-E)VK(d- L)DAE(d-F)	GJ	P			K	GY	368
	Fm- K	D		P	JG	S(d-E)VK(d- L)DAE(d-F)	GJ	P			K	GY	369
	K	D		B	JG	SEVN <u>L</u> DAE F	GJ	P			K	DDY	370
	K	D		B	JG	SEVK <u>L</u> DAE F	GJ	P			K	DDY	371
NATIVE AMYLOID													
	K	D		B	JG	SEVK <u>M</u> DA EF	GJ	P			K	DDY	372
CATHESPSIN G													
	K	D		B	JG	SEVK <u>M</u> DD EF	GJ	P			K	DDY	373
	K	D		B	JG	SEVN <u>L</u> DDE F	GJ	P			K	DDY	374
APP[709-710]													
	K	D		B	JG	GVV <u>I</u> ATVI VIT	GJ	P			K	DDY	375
APP[708-719]													
	K	D		B	JG	YGVV <u>I</u> ATV IVIT	GJ	P			K	DDY	376
APP[711-716]													
	K	D		B	JG	V <u>I</u> ATVI	GJ	P			K	DDY	377
APP[708-713]													

	K	D		B	JB	YGVVIA	GJ	P			K	DDY	378
PSA Sg1													
	K	D		B	JJ	QQLLHN	JJ	P			K		379
	K	D		B	JG	QQLLHN	GJ	P			K		380
	K	D		B	G	QQLLHN	G	P			K		381
	K	D		B		QQLLHN		P			K		382
PSA Sg2													
	K	D		B	JJ	SIQYTY	JJ	P			K		383
	K	D		B	JG	SIQYTY	GJ	P			K		384
	K	D		B	G	SIQYTY	G	P			K		385
	K	D		B		SIQYTY		P			K		386
PSA Sg3													
	K	D		B	JJ	SSQYSN	JJ	P			K		387
	K	D		B	JG	SSQYSN	GJ	P			K		388
	K	D		B	G	SSQYSN	G	P			K		389
	K	D		B		SSQYSN		P			K		390
PSA Sg4													
	K	D		B	JJ	SSIYSQ	JJ	P			K		391
	K	D		B	JG	SSIYSQ	GJ	P			K		392
	K	D		B	G	SSIYSQ	G	P			K		393
	K	D		B		SSIYSQ		P			K		394
Cathepsin D substrates (preferably with diethylrhodamine fluorophore, note fmoc (Fm) is optional)													
	Fm-K	D		P	JG	SEVNLDAE F	GJ	P			K	GY	395
Caspase-9													
	Fm-K	D		P	JG	LEHDGIN	GJ	P			K	GY	396
Caspase-8													
	Fm-K	D		P	JG	LETDGIN	GJ	P			K	GY	397
Caspase-1													
	Fm-	D		P	JG	WEHDGIN	GJ	P			K	GY	398

	K												
	Fm-K	D		P	JG	YVHDG	J	P			K	GY	399
	Fm-K	D		P	JG	YVHDGIN	GJ	P			K	GY	400
	Fm-K	D		P	JG	YVHDA		P			K	GY	401
Granzyme B													
	Fm-K	DP			JG	IEPDS	GJ	P			K	GY	402
Collagenase													
	Fm-K	DP			JG	PLGIAGI	GJ	P			K	GY	403
HIV-1 protease													
	Fm-K	DP			JG	SQNYPIVQ	GJ	P			K	GY	404
Hepatitis C protease													
	Fa-K	DP			JG	EDVVCCS	GJ	P			K	GY	405

* In certain embodiments, the Fm or Fa groups identified in the above sequences are optional or can be substituted with other hydrophobic groups. Conversely any of the sequences listed without a hydrophobic group can have one added. In addition, in certain embodiments, the carboxyl terminal amino acid can have the carboxylic acid group replaced with an amide